

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Lee, Wen-Hwa  
Shepard, H. Michael  
Gregory, Richard J.  
Wills, Ken N.  
Maneval, Daniel C.  
Lee, Eva  
Goodrich, David  
Wang, Nan-Ping

(ii) TITLE OF INVENTION: Cell Cycle Controlling Compositions and Methods of Use

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, Eighth Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/472,760  
(B) FILING DATE: 07-JUN-1995  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/951,947  
(B) FILING DATE: 28-SEP-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/276,041  
(B) FILING DATE: 14-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/764,714  
(B) FILING DATE: 24-SEP-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/265,829  
(B) FILING DATE: 31-OCT-1988

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/225,099  
(B) FILING DATE: 08-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/079,207  
(B) FILING DATE: 17-JUN-1993

- (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/914,039
    - (B) FILING DATE: 14-JUL-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/550,877
    - (B) FILING DATE: 11-JUL-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/058,784
    - (B) FILING DATE: 07-MAY-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/906,008
    - (B) FILING DATE: 26-JUN-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/553,905
    - (B) FILING DATE: 16-JUL-1990
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/306,513
    - (B) FILING DATE: 13-SEP-1994
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/121,108
    - (B) FILING DATE: 13-SEP-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/956,472
    - (B) FILING DATE: 02-OCT-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/126,810
    - (B) FILING DATE: 24-SEP-1993
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/778,510
    - (B) FILING DATE: 17-OCT-1991
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Bastian, Kevin L.
    - (B) REGISTRATION NUMBER: 34,774
    - (C) REFERENCE/DOCKET NUMBER: 17726A-000410US
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (415) 576-0200
    - (B) TELEFAX: (415) 576-0300
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2994 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 139..2922  
 (D) OTHER INFORMATION: /product= "RB protein"  
       /note= "retinoblastoma (RB) gene"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 1273..2922  
 (D) OTHER INFORMATION: /note= "truncated RB protein fragment  
       p56-RB"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 2887..2922  
 (D) OTHER INFORMATION: /note= "RB protein C-terminal peptide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|  |     |
|--|-----|
| TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG   | 60  |
| GGCGTGCCCC GCGTCGCGGC GCGTCGTCCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC | 120 |
| CCGCCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC   | 171 |
| Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala                        |     |
| 1                  5                  10                           |     |
| ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC        | 219 |
| Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro            |     |
| 15                20                25                             |     |
| CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT    | 267 |
| Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro    |     |
| 30                35                40                             |     |
| CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA    | 315 |
| Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala    |     |
| 45                50                55                             |     |
| TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG    | 363 |
| Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp    |     |
| 60                65                70                75           |     |
| TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT    | 411 |
| Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr    |     |
| 80                85                90                             |     |
| ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA    | 459 |
| Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala        |     |
| 95                100               105                            |     |
| GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC    | 507 |
| Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn    |     |
| 110               115               120                            |     |
| ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT    | 555 |
| Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp    |     |
| 125               130               135                            |     |

|   |      |
|---|------|
| ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT<br>Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr<br>140 145 150 155 | 603  |
| GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT<br>Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu<br>160 165 170     | 651  |
| ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT<br>Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser<br>175 180 185     | 699  |
| GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG<br>Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly<br>190 195 200     | 747  |
| GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG<br>Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met<br>205 210 215     | 795  |
| CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC<br>Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu<br>220 225 230 235 | 843  |
| AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA<br>Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg<br>240 245 250     | 891  |
| ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA<br>Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu<br>255 260 265     | 939  |
| GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT<br>Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys<br>270 275 280     | 987  |
| AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT<br>Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe<br>285 290 295     | 1035 |
| ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA<br>Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu<br>300 305 310 315 | 1083 |
| AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA<br>Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu<br>320 325 330     | 1131 |
| GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT<br>Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser<br>335 340 345     | 1179 |
| ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT<br>Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp<br>350 355 360     | 1227 |
| GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG<br>Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met<br>365 370 375     | 1275 |
| AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA   | 1323 |



| 620   | 625 | 630 | 635 |      |
|---|-----|-----|-----|------|
| TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT<br>Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr<br>640 | 645 | 650 |     | 2091 |
| AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA<br>Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu<br>655 | 660 | 665 |     | 2139 |
| CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT<br>Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu<br>670 | 675 | 680 |     | 2187 |
| TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT<br>Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His<br>685 | 690 | 695 |     | 2235 |
| TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG<br>Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys<br>700 | 705 | 710 | 715 | 2283 |
| AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT<br>Asn Ile Asp Leu Lys Phe Lys Ile Val Thr Ala Tyr Lys Asp Leu<br>720     | 725 | 730 |     | 2331 |
| CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG<br>Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu<br>735 | 740 | 745 |     | 2379 |
| GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA<br>Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg<br>750 | 755 | 760 |     | 2427 |
| CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG<br>Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu<br>765 | 770 | 775 |     | 2475 |
| TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA<br>Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser<br>780 | 785 | 790 | 795 | 2523 |
| CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT<br>Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser<br>800 | 805 | 810 |     | 2571 |
| CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA<br>Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro<br>815 | 820 | 825 |     | 2619 |
| AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG<br>Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu<br>830 | 835 | 840 |     | 2667 |
| AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC<br>Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu<br>845 | 850 | 855 |     | 2715 |
| AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA<br>Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu<br>860 | 865 | 870 | 875 | 2763 |

|   |      |
|---|------|
| CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC<br>Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu<br>880                    885                    890 | 2811 |
| CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT<br>Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr<br>895                    900                    905 | 2859 |
| CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA<br>Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser<br>910                    915                    920 | 2907 |
| AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT<br>Asn Lys Glu Glu Lys<br>925   | 2962 |
| GGATTTCATTG TCTCTCACAG ATGTGACTGT AT  | 2994 |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|   |
|---|
| Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala<br>1                    5                    10                    15       |
| Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp<br>20                    25                    30                               |
| Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu<br>35                    40                    45                           |
| Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu<br>50                    55                    60                           |
| Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys<br>65                    70                    75                    80     |
| Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys<br>85                    90                    95                           |
| Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu<br>100                    105                    110                        |
| Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val<br>115                    120                    125                        |
| His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val<br>130                    135                    140                        |
| Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala<br>145                    150                    155                    160 |

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
                  165                 170                 175  
  
 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
                  180                 185                 190  
  
 Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met  
                  195                 200                 205  
  
 Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp  
                  210                 215                 220  
  
 Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys  
                  225                 230                 235                 240  
  
 Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly  
                  245                 250                 255  
  
 Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg  
                  260                 265                 270  
  
 Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val  
                  275                 280                 285  
  
 Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly  
                  290                 295                 300  
  
 Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg  
                  305                 310                 315                 320  
  
 Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe  
                  325                 330                 335  
  
 Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu  
                  340                 345                 350  
  
 Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Val Asn Val  
                  355                 360                 365  
  
 Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln  
                  370                 375                 380  
  
 Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu  
                  385                 390                 395                 400  
  
 Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu  
                  405                 410                 415  
  
 Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys  
                  420                 425                 430  
  
 Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu  
                  435                 440                 445  
  
 Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu  
                  450                 455                 460  
  
 Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn  
                  465                 470                 475                 480  
  
 Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala

485

490

495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu  
 500 505 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe  
 515 520 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg  
 530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser  
 545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser  
 565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu  
 580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser  
 595 600 605

Pro Val Arg Ser Pro Lys Lys Gly Ser Thr Thr Arg Val Asn Ser  
 610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys  
 625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg  
 645 650 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu  
 660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu  
 675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met  
 690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys  
 705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln  
 725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Tyr Asp Ser Ile  
 740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile  
 755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His  
 770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro  
 785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser  
 805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu  
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile  
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu  
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu  
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys  
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln  
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
915 920 925